

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BRUST, Stefan  
KNAPP, Stefan  
GERKEN, Manfred  
GUERTLER, Lutz
- (ii) TITLE OF INVENTION: Peptides derived from a retrovirus of  
the HIV group, and their use
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Foley & Lardner
  - (B) STREET: 3000 K Street, N.W., Suite 500
  - (C) CITY: Washington
  - (D) STATE: D.C.
  - (E) COUNTRY: USA
  - (F) ZIP: 20007-5109
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/394,021
  - (B) FILING DATE: 23-FEB-1995
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: DE P 44 05 810.1
  - (B) FILING DATE: 23-FEB-1994
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: SANDERCOCK, Colin G.
  - (B) REGISTRATION NUMBER: 31,298
  - (C) REFERENCE/DOCKET NUMBER: 58315/106/BEAK
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (202)672-5300
  - (B) TELEFAX: (202)672-5399
  - (C) TELEX: 904136

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 29
  - (D) OTHER INFORMATION: /note= "Xaa represents Cys or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION: /note= "Xaa represents Cys or Ser"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Val Trp Gly Ile Arg Gln Leu Arg Ala Arg Leu Gln Ala Leu Glu Thr
1           5           10           15
Leu Ile Gln Asn Gln Gln Arg Leu Asn Leu Trp Gly Xaa Lys Gly Lys
20           25           30
Leu Ile Xaa Tyr Thr Ser Val Lys Trp Asn Thr Ser Trp Ser Gly Arg
35           40           45

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Asn Gln Gln Arg Leu Asn Leu Trp Gly Cys Lys Gly Lys Leu Ile Cys
1           5           10           15
Tyr Thr Ser Val Lys Trp Asn
20

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Arg Leu Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Arg Leu Asn
1           5           10           15
Leu Trp Gly Cys Lys Gly Lys Leu Ile Cys
20           25

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Leu Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Arg Leu Asn  
1 5 10 15  
Leu Trp Gly Ser Lys Gly Lys Leu Ile Ser  
20 25

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys  
1 5 10 15  
Thr Thr Ala Val Pro Trp Asn  
20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Ile Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly  
1 5 10 15  
Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys  
20 25

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Arg Ile Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly  
1 5 10 15

Ile Trp Gly Ser Ser Gly Lys Leu Ile Ser  
20 25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGTGTGGTAC CGCAGCGGCA ACAGCGCTGA CG

32

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTGTGTCTAG TTTAGTTATG TCAAACCAAT TC

32

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 146 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Ala Thr Ala Leu Thr Val Arg Thr His Ser Val Leu Lys Gly Ile  
1 5 10 15  
Val Gln Gln Gln Asp Asn Leu Leu Arg Ala Ile Gln Ala Gln Gln His  
20 25 30  
Leu Leu Arg Leu Ser Val Trp Gly Ile Arg Gln Leu Arg Ala Arg Leu  
35 40 45  
Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Arg Leu Asn Leu Trp  
50 55 60  
Gly Cys Lys Gly Lys Leu Ile Cys Tyr Thr Ser Val Lys Trp Asn Thr  
65 70 75 80  
Ser Trp Ser Gly Arg Tyr Asn Asp Asp Ser Ile Trp Asp Asn Leu Thr  
85 90 95

Trp Gln Gln Trp Asp Gln His Ile Asn Asn Val Ser Ser Ile Ile Tyr  
100 105 110  
Asp Glu Ile Gln Ala Ala Gln Asp Gln Gln Glu Lys Asn Val Lys Ala  
115 120 125  
Leu Leu Glu Leu Asp Glu Trp Ala Ser Leu Trp Asn Trp Phe Asp Ile  
130 135 140  
Thr Lys  
145

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Val Ser Leu Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile  
1 5 10 15  
Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His  
20 25 30  
Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val  
35 40 45  
Leu Ala Val Glu Arg Tyr Leu Arg Asp Gln Gln Leu Leu Gly Ile Trp  
50 55 60  
Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala  
65 70 75 80  
Ser Trp Ser Asn Lys Ser Leu Glu Asp Ile Trp Asp Asn Met Thr Trp  
85 90 95  
Met Gln Trp Glu Arg Glu Ile Asp Asn Tyr Thr Asn Thr Ile Tyr Thr  
100 105 110  
Leu Leu Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu  
115 120 125  
Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Ser Ile Thr  
130 135 140  
Asn  
145